

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 12, 2003, 22:48:30 ; Search time 5084 Seconds  
(without alignments)  
13027.084 Million cell updates/sec

Title: US-10-054-678-1  
Perfect score: 2725  
Sequence: 1 tcagtcgtggccagcctg.....aagtcacacttggctggc 2725

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 120 summaries

Database :

EST:\*

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_hc.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_hc.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

19: em\_gss\_pln.\*

20: em\_gss\_vrt.\*

21: em\_gss\_fun.\*

22: em\_gss\_mam.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rod.\*

26: em\_gss\_pbg.\*

27: em\_gss\_vrl.\*

28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	980.6	36.0	1201	9	AL517921
2	953.2	35.0	1201	13	BX404004
3	927.2	34.0	1192	9	AL515786
4	900.6	33.0	1201	9	AL515787

78	397.8	14.6	638	12	BG965999	BG965999 602829793
79	390	14.3	508	9	AW78401	AW78401 119530 MA
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82	323.4	11.9	440	10	BE314345	BE314345 601147067
83	310	11.4	694	13	BX416107	BX416107 BX416107
84	304.2	11.2	542	10	BF525224	BF525224 UT-R-AB1-
85	300.6	11.0	311	9	AA349106	AA349106 EST55691
86	271	9.9	423	9	AI386204	AI386204 mg64C06.Y
87	271	9.9	434	9	AA142680	AA142680 mg64C06.X
88	262.2	9.6	1289	10	BF316992	BF316992 60193955
89	260.6	9.6	477	14	CA364439	CA364439 639338 NC
90	238.2	8.7	1108	13	BU384712	BU384712 603858882
91	229	8.4	315	12	BI976348	BI976348 485196 MA
92	211.6	7.8	254	14	T27961	T27961 EST21967 Hu
93	207.6	7.6	338	13	BY127879	BY127879 BY127879
94	175.8	6.5	2160	11	AK081586	AK081586 Mus muscu
95	175.8	6.5	2884	11	AK030274	AK030274 Mus muscu
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97	164.4	6.0	167	10	BF311282	BF311282 601898667
98	164	6.0	179	9	AA329415	AA329415 EST33021
99	151.8	5.6	168	10	BF314505	BF314505 601900794
c 100	151.4	5.6	291	9	AW505180	AW505180 UT-HF-BN0
c 101	143.2	5.3	222	14	T11501	T11501 CHR90067 Ch
c 102	141.2	5.2	624	28	AZ366751	AZ366751 IM0116D11
103	125.4	4.6	127	10	BE261275	BE261275 601148836
104	125.4	4.6	127	10	BE261544	BE261544 601149214
105	123.4	4.5	837	13	BU377516	BU377516 603813070
106	116.4	4.3	611	9	AV222200	AV222200 AV222200
107	103.4	3.8	129	10	BE313872	BE313872 601148905
108	103	3.8	321	9	AI256710	AI256710 ui30D04.Y
109	103	3.8	519	4	EX512116	EX512116 R2PD Mus
110	102	3.7	886	13	BU543008	BU543008 AGENCOURT
111	101.2	3.7	915	13	EX390150	EX390150 EX390150
112	98	3.6	801	13	EX315600	EX315600 BX315600
113	90.6	3.3	830	10	BF159611	BF159611 601767217
114	87	3.2	532	12	BI514653	BI514653 BB160015B
c 115	86.4	3.2	489	12	BI320021	BI320021 ie46H03.Y
c 116	84.8	3.1	961	29	CNS03RBC	AL257025 Tetraodon
c 117	84.2	3.1	734	13	BX261734	BX261734 BX261734
c 118	83.8	3.1	520	9	AI892295	AI892295 mm25G09.Y
c 119	82.6	3.0	704	14	CD218235	CD218235 pgrin.pk0
120	82.2	3.0	981	10	BF167377	BF167377 601773665

ALIGNMENTS

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LOCUS	AL517921	CS0DA004YB14	5-PRIME, mRNA	sequence.	
DEFINITION	AL517921	AL517921 Homo sapiens NEUROBLASTOMA	Homo sapiens	cDNA clone	
ACCESSION	AL517921	AL517921	AL517921	AL517921	
VERSION	AL517921.2	GI:30535710	GI:30535710	GI:30535710	
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1	(bases 1 to 1201)			
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
COMMENT	On Feb 13, 2001 this sequence version replaced gi:12781414.				
	Contact: Genoscope				
	Genoscope - Centre National de Sequencage				
	BP 191 91006 EVRY cedex - France				
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr				
	Library was constructed by Life Technologies, a division of				
	Invitrogen. This sequence belongs to sequence cluster 5245.f For				
	more information about this cluster, see				
	http://www.genoscope.cns.fr/				

cgi-bin/cluster.cgi?seq=CS0DA004DA07QP1&cluster=5245.f. Contact :  
Feng Liang Email : fliang@life.techn.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0DA004DA07QP1.  
Location/Qualifiers  
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/clone="CS0DA004YB14"  
/tissue type="NEUROBLASTOMA"  
/clone lib="Homo sapiens NEUROBLASTOMA"  
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with a NotI-oligo(dT) primer. Five prime end enriched, into  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pcMVSPORT 6 vector.  
Library was not normalized."  
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Best Local Similarity 91.2%; Pred. No. 4.5e-202;  
Matches 1029; Conservative 44; Mismatches 51; Indels 4; Gaps 4;  
Qy 88 TGGTGGCCGACATGACAGGCTCGGCTCCCGGTGAGAGCCCTCCCTCATCATCCCC 147  
Db 66 TGGTGGCCGACATGACAGGCTCGGCTCCCGGTGAGAGCCCTCCCTCATCATCCCC 125  
Qy 148 TGGACCCGAGGAGGCTCCCTGGAGCTCTCATGGAATGTGAGTACACCCAGAGGCCATCC 207  
Db 126 TGGACCCGGA-GGGTCCCTGGAGCTCTCATGGAATGTGAGTACACCCAGAGGCCATCC 184  
Qy 208 ATTTCAGCTCTCTGTCGAGAGCTCAAGGCTGGCGTCTCTGTTTGGAGTGTCCAGCGTG 267  
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Qy 328 CGGACCCCTGGAGTGAACCAAGAGGCGACATCCACCTGGATCCCAAGAGGACTACAGC 387  
Db 305 CGGACCCCTGGAGTGAACCAAGAGGCGACATCCACCTGGATCCCAAGAGGACTACAGC 364  
Qy 388 TGGTGGAGTGCAGAGGACCCAGAGGCTGACCTGCTCTTTTCAAGAGGCCCTTTGGCA 447  
Db 365 TGGTGGAGTGCAGAGGACCCAGAGGCTGACCTGCTCTTTTCAAGAGGCCCTTTGGCA 424  
Qy 448 CTGCGACCCCAAGGATTACCTCATTTGAAGAGGCGACTGTCACCTTGGTCTAGGGATCC 507  
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Qy 628 CCATGGAGTCCAAGCTCCCAATATCCAGATCCCGAGCCAGAGACCACTACTGCTGCT 687  
Db 605 CCATGGAGTCCAAGCTCCCAATATCCAGATCCCGAGCCAGAGACCACTACTGCTGCT 664  
Qy 688 ACATTAAGGAGCTTCCAAAGGGCTTCTCTCGGCACCAATATCAAGTACGAGCCCATCG 747  
Db 665 ACATTAAGGAGCTTCCAAAGGGCTTCTCTCGGCACCAATATCAAGTACGAGCCCATCG 724  
Qy 748 TCACCAAGGGCAATAGAGCCCTTTGTCACCAATGGAAGTCTTCAGTGGCGCCCGCAGA 807  
Db 725 TCACCAAGGGCAATAGAGCCCTTTGTCACCAATGGAAGTCTTCAGTGGCGCCCGCAGA 784  
Qy 808 TGGACAGCGTCCCCCCTTTCAGCGGGCTTCCAGAGTGAAGTGAACCCGAGCCGCTCA 867





cgi-bin/cluster.cgi?seq=CS0DA001CF06QPl&cluster=5245.f. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0DA001CF06QPl.

## FEATURES

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/organism="Homo sapiens"  
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with a NotI-oligo (dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."  
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Query Match 33.0%; Score 900.6; DB 9; Length 1201;  
Best Local Similarity 95.6%; Pred. No. 1e-184;  
Matches 980; Conservative 5; Mismatches 32; Indels 8; Gaps 6;  
Qy 1 TCAGTCGTCGGCCAGCAGCTGCGCGCCGCCACATGCGGAGGCGAGCTTCATGTACAGCA 60  
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Db 133 CAGCAGTGGCCATCTTCTGTGTATCTCTGTGGCGGCGACTGCGAGGCTCGGCTCCCGTG 192  
Qy 121 AGAGCCCCCTCCCTATCACATCCCTCTGGACCGGAGGGTCCCTGGAGCTTCATGGA 180  
Db 193 AGAGCCCCCTCCCTATCACATCCCTCTGGACCGGAGGGTCCCTGGAGCTTCATGGA 251  
Qy 181 ATGTAGTACACCCAGGAGGCCATTCATTTCCAGTCTCTGGTGGGAGGCTCAAGGCTG 240  
Db 252 ATGTAGTACACCCAGGAGGCCATTCATTTCCAGTCTCTGGTGGGAGGCTCAAGGCTG 311  
Qy 241 GCCTCTGTTTGGATGTCACCGCTGCGAGCTTGAGACGAGATCTCGTGTGCTCT 300  
Db 312 CGCTCTGTTTGGATGTCACCGCTGCGAGCTTGAGACGAGATCTCGTGTGCTCT 371  
Qy 301 GGACCGATGGGACACTGCCTATTTTGGGACGCTTGAGTGACAGAGGGGCGAGATCC 360  
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Qy 361 ACCTGGATCCCGCAGAGACTACCACTGTCTGAGGTGCGAGGACCCAGAGGCTCTGA 420  
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Db 492 CCCTGCTTTTCAAGAGCCCTTTGGCACCTGCGACCCCAAGGATTAATCTTGAAGACG 551  
Qy 481 GCATGTCCTTCTACGGATCTCTGGAGGAGCGGTTCCTGGTCACTGAGGCGCATCA 540  
Db 552 GCATNTCCACTTGGTCTACGGGATCTCTGGAGGAGCGGTTCCTGGTCACTGAGGCGCATCA 611  
Qy 541 ACGGCTCGGGCTCAGATGGGCTGCGAGGGTGCAGGCTCTCTGAAGCCCAATATCCCG 600  
Db 612 ACGGCTCGGGCTCAGATGGGCTGCGAGGGTGCAGGCTCTCTGAAGCCCAATATCCCG 671  
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Qy 660 CCCAGCAGGAGACCACTACTGTGTGTACATTAAAGAGCTTCCAAAGGGCTTCTCTCGG 719  
Db 732 CCCAGCAGGAGACCACTACTGTGTGTACATTAAAGAGCTTCCAAAGGGCTTCTCTCGG 791  
Qy 720 CACCACATTATCAAGTACGAGCCCATCGTCACCAAGGGCAATGAGGCGCTTGTCCACCAC 779

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Db 852 ATGGAAGTCTTCCAGTCGCGCCCGGAGATGACAGCGTCCCCCACTTCAGCGGGCCCTGC 911  
Qy 840 GACTCCAGATGAACCCGACCGCTCAACTACTTACGCGCCACAGTGTGCGCGCTTGGGCC 899  
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Qy 900 CTGGGTCCCAAGCATTTTACTACCCAGAGAACCGCCCTTCTCTCGGGGTTCAGGG 959  
Db 972 CTGGGTG-CAAGGCATTTTACTACCCAGAGAA-SCGGCTTGTCTTTCGGGGTCT--AGG 1027  
Qy 960 TCCTCCAGATATCTCCGCTTGGAGTTTCACTTACCACAAACCCACTGGTGATAGAAGGACGA 1019  
Db 1028 GTCTCCAGATATCTCGC--TGGATTTCACTACAAAACCACTGGTGAWAAGGGAACGM 1085  
Qy 1020 AACGA 1024  
Db 1086 TCCCA 1090  
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LOCUS BX365876 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens  
DEFINITION CDNA clone CS0DC006YB08 5-PRIME, mRNA sequence.  
ACCESSION BX365876  
VERSION BX365876.1 GI:30378944  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 989)  
Li, W.B., Gruber, C., Jesses, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 5245.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS1DC002ZD07QPl&cluster=5245.f. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS1DC002ZD07QPl.  
FEATURES  
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primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoRV  
sites of the pCMVSPORT 6 vector. Library was normalized."  
BASE COUNT 187 a 338 c 272 g 183 t 9 others  
ORIGIN  
Query Match 32.5%; Score 885.2; DB 13; Length 989;  
Best Local Similarity 98.0%; Pred. No. 2.1e-181;  
Matches 898; Conservative 7; Mismatches 10; Indels 1; Gaps 1;  
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Db      58 GCATGTGGAAGAGTGTGTCGTGCTCCATCGGAGATGTGCTCATCACCTCTCGCAGCT 117
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QY      1453 GTGTCAACTACGTGCACTACTACCCCCAGACGAGCTGGAGCTCTGCAAGACGGCTGTGG 1512
Db      178 GTGTCAACTACGTGCACTACTACCCCCAGACGAGCTGGAGCTCTGCAAGAGAGATGTCT 236
QY      1513 ACGCCGGCTTCCTGCAGAACTACTTCCACCTCATCAACAGGTTCAACAAACAGGAGATGTCT 1572
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QY      1573 GCACCTGCCCTCAGGGGTCGGTGTCTCAGCAGTTTCACTCTGTTCCTTGAATCTCTTCA 1632
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QY      1633 ACCGCGACGTACTGAAGGCCCTGTACAGCTTTCGCGCCATCTCCATGCACTGCAACAAGT 1692
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QY      1873 TGCTGTCCCTGTGGGCTCACACCGGCATGTGCATCTACTCTGCGACGATCCCATGGA 1932
Db      597 TGCTGTCCCTGTGGGCTCACACCGGCATGTGCATCTACTCTGCGACGATCCCATGGA 656
QY      1933 ACAGCCCTGCAGCCACAGGATGAAGGGCCAGACACGCCCCCTGCTGAGACACCGGTCC 1992
Db      657 ACAGCCCTGCATGCCACAGGATGAAGGGCCAGACACGCCCCCTGCTGAGAMCAGGTCC 716
QY      1993 AATCCAGCCTTCTTCCCCAGGGTCCCTTCATGGCTGAGAGGGTGTGGGTGCCCCCTGTTG 2052
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## RESULT 6

AL526121

LOCUS

DEFINITION AL526121 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens

cDNA clone CS0DC015YD20 5-PRIME, mRNA sequence.

ACCESSION AL526121

VERSION AL526121.2

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1. (bases 1 to 993)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished

On Feb 13, 2001 this sequence version replaced gi:12789614.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5245.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DC015DB10Q1&cluster=5245.f. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DC015DB10Q1.

FEATURES  
source

1. .993

/organism="Homo sapiens"

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/db\_xref="taxon:9606"

/clone="CS0DC015YD20"

/tissue\_type="NEUROBLASTOMA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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## ORIGIN

Query Match 32.3%; Score 879; DB 9; Length 993;

Best Local Similarity 98.3%; Pred. No. 4.6e-180;

Matches 909; Conservative 9; Mismatches 4; Indels 3; Gaps 3;

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Db      132 CAGCAGTGCCCATCTTCTCGGTTCATCTCGTGGCGGCTGCGAGGCTCGGCTCCCGGTG 191
QY      121 AGAGCCCCCTCCCTATACATCCCTCCCGAGCCCGGAGGGGTCCCTGGAGCTCTCATGGA 180
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Db      311 GGTCTCTGTTTGGGATGTCCGACCGTGGCGAGCTTCAGAACCGCAGATCTCGTGTGCTCT 370
QY      301 GGACCGATGGGACACTGCTATTTTGGGACGCTGGAGTGCACAGAGGGGCGAGATCC 360
Db      371 GGACCGATGGGACACTGCTATTTTGGGACGCTGGAGTGCACAGAGGGGCGAGATCC 430
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Db      431 ACCTGATCCCGACGAGGACTACAGCTGTCAGAGTGTCAGAGGACCCAGAGGCTGA 490
QY      421 CCTGCTCTTTCAAGAGGCTTCTGGCACCTGCGACCCCAAGGATTAACCTCATTGAAGACG 480
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QY      481 GCATCTGCATTTGGTCTACGGGATCTCTGGAGAGCCGTTCCGGTCACTGGAGGCCATCA 540
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 QY 671 AACCGGAGTTGCCCTCAGACGGCTGCACCATGAGGTCCAGCTCCCAATATCCAGATCC 730  
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 QY 661 CCAGCCAGGAGACCACTGCTACTGCTACATTAAGGAGCTTCCAAAGGGCTTCTCTCGGC 720  
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 QY 731 CCAGCCAGGAGACCACTGCTACTGCTACATTAAGGAGCTTCCAAAGGGCTTCTCTCGGC 790  
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 QY 791 ACCAATTATCAAGTACGAGCCCATGCTCAACAGGGCAATGAGCCCTTGTCCACCACA 850  
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 Db |||||  
 QY 851 TGGAGTCTTCCAGTGGCGCCCGGAGATGGACAGGT - CCCACTTCAGCGGGSCCTGCG 909  
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 QY 841 ACTCCAAGATGAACCCGACCGCTCAACTACTGCGGCACGTGCTGCGCGCTGGGCC 900  
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 QY 910 ACTCCAAGATGAACCCGACCGCTCAACTACTGCGGCACGTGCTGCGCGCTGGGCC 969  
 Db |||||  
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## RESULT 7

AL514764  
 LOCUS  
 DEFINITION  
 AL514764 Homo sapiens NEUROBLASTOMA linear EST 08-MAY-2003  
 CLOBB0152E02 5-PRIME, mRNA sequence.  
 AL514764  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 974)  
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished  
 On Feb 13, 2001 this sequence version replaced gi:12778257.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 5245.f For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cwuser.cgi?seq=CLOBB0152E02R1&cluster=5245.f. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CLOBB0152E02R1.  
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 the NotI and EcoRV sites of the pCMVSPORT 6 vector.  
 Library was not normalized."  
 193 a 320 c 280 g 178 t 3 others

## BASE COUNT

RESULT 8  
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## ORIGIN

Query Match 32.2%; Score 878.4; DB 9; Length 974;  
 Best Local Similarity 99.7%; Pred. No. 6.1e-180;  
 Matches 901; Conservative 0; Mismatches 1; Indels -2; Gaps 2;  
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 QY 121 AGAGCCCCCTCCCTATCACATCCCTTGACCGGAGGGGTCCCTGAGCTCTCATGGA 180  
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## FEATURES

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 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed  
 with a NotI-oligo(dT) primer. Five prime end enriched,  
 double-strand cDNA was digested with NotI and cloned into  
 the NotI and EcoRV sites of the pCMVSPORT 6 vector.  
 Library was not normalized."  
 193 a 320 c 280 g 178 t 3 others



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LOCUS       AL526065                980 bp    mRNA    linear    EST 23-MAY-2003
DEFINITION   CDNA clone CS0DC015Y20 3-PRIME, mRNA sequence.
ACCESSION    AL526065
VERSION      AL526065.2  GI:31063926
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  1 (bases 1 to 980)
  Full-length cDNA libraries and normalization
  Unpublished
  On Feb 13, 2001 this sequence version replaced gi:12789558.
CONTACT      Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5245.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC015DB10NP1&cluster=5245.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC015DB10NP1.
Location/Qualifiers
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  /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
  /note="1st strand cDNA was primed with a NotI-oligo(dT)
  primer. Five prime end enriched, double-strand cDNA was
  digested with Not I and cloned into the Not I and EcoR V
  sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT   187 a 263 c 337 g 153 t    40 others
ORIGIN
Query Match      32.2%; Score 877; DB 9; Length 980;
Best Local Similarity 93.4%; Pred. No. 1.2e-179;
Matches 902; Conservative 26; Mismatches 36; Indels 2; Gaps 2;
QY 1425 GGGGGCTTGGGATCTCGGAGGAGATGTGTCAACTACGTGACACTACTACCCCGACAGC 1484
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DB 680 CTGACGCCCTCGCCCAAGGTCATCTCCACACTGGAAGAGCCACACAGTGGCCCCACC 621
QY 1785 AGCCAGGGCGCAAGCCCTGCTGCCCCACCGTTGTGACAGATTGGTGGGGGCAAGAGCTGA 1844
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LOCUS       AL524359                948 bp    mRNA    linear    EST 22-MAY-2003
DEFINITION   CDNA clone CS0DC006YB08 5-PRIME, mRNA sequence.
ACCESSION    AL524359
VERSION      AL524359.2  GI:31042620
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  1 (bases 1 to 948)
  Full-length cDNA libraries and normalization
  Unpublished
  On Feb 13, 2001 this sequence version replaced gi:12787852.
CONTACT      Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5245.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC006DA04QPI&cluster=5245.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC006DA04QPI.
Location/Qualifiers
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  /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
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  primer. Five prime end enriched, double-strand cDNA was
  digested with Not I and cloned into the Not I and EcoR V
  sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT   187 a 263 c 337 g 153 t    40 others
ORIGIN
Query Match      32.2%; Score 877; DB 9; Length 980;
Best Local Similarity 93.4%; Pred. No. 1.2e-179;
Matches 902; Conservative 26; Mismatches 36; Indels 2; Gaps 2;
QY 1425 GGGGGCTTGGGATCTCGGAGGAGATGTGTCAACTACGTGACACTACTACCCCGACAGC 1484
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DB 680 CTGACGCCCTCGCCCAAGGTCATCTCCACACTGGAAGAGCCACACAGTGGCCCCACC 621
QY 1785 AGCCAGGGCGCAAGCCCTGCTGCCCCACCGTTGTGACAGATTGGTGGGGGCAAGAGCTGA 1844
DB 620 AGCCAGGGCGCAAGCCCTGCTGCCCCACCGTTGTGACAGATTGGTGGGGGCAAGAGCTGA 561

LOCUS       AL524359                948 bp    mRNA    linear    EST 22-MAY-2003
DEFINITION   CDNA clone CS0DC006YB08 5-PRIME, mRNA sequence.
ACCESSION    AL524359
VERSION      AL524359.2  GI:31042620
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  1 (bases 1 to 948)
  Full-length cDNA libraries and normalization
  Unpublished
  On Feb 13, 2001 this sequence version replaced gi:12787852.
CONTACT      Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5245.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC006DA04QPI&cluster=5245.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC006DA04QPI.
Location/Qualifiers
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  /clone="CS0DC006YB08"
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  /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
  /note="1st strand cDNA was primed with a NotI-oligo(dT)
  primer. Five prime end enriched, double-strand cDNA was
  digested with Not I and cloned into the Not I and EcoR V
  sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT   187 a 263 c 337 g 153 t    40 others
ORIGIN
Query Match      32.2%; Score 877; DB 9; Length 980;
Best Local Similarity 93.4%; Pred. No. 1.2e-179;
Matches 902; Conservative 26; Mismatches 36; Indels 2; Gaps 2;
QY 1425 GGGGGCTTGGGATCTCGGAGGAGATGTGTCAACTACGTGACACTACTACCCCGACAGC 1484
DB 979 GTGGGGYTTCCBWTCTCTGGGMCCTKIGTGTGCGCMCGTGCMTCTCTTCCCCCGMGC 920
QY 1485 CAGTGGAGCTTCGCAAGACGGCTGTGGACCGCGGCTTCTCGAGAAGTACTTCCACCTC 1544
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DB 799 TTCACTCTCTTCCCTGGMACTCTTCAACCGCGAGTACTGAAGCGCTGT-TACMGTC 741
QY 1665 GCGCCCATCTCCATGCACTGCACAGATCTTCAGCGCTCGCTTCAGGGTGAATGGAAC 1724
DB 740 GCGCCCATCTCCATGCACTGCACAGATCTTCAGCGCTCGCTTCAGGGTGAATGGAAC 681
QY 1725 CTGACGCCCTCGCCCAAGGTCATCTCCACACTGGAAGAGCCACACAGTGGCCCCACC 1784
DB 680 CTGACGCCCTCGCCCAAGGTCATCTCCACACTGGAAGAGCCACACAGTGGCCCCACC 621
QY 1785 AGCCAGGGCGCAAGCCCTGCTGCCCCACCGTTGTGACAGATTGGTGGGGGCAAGAGCTGA 1844
DB 620 AGCCAGGGCGCAAGCCCTGCTGCCCCACCGTTGTGACAGATTGGTGGGGGCAAGAGCTGA 561
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/organism="Homo sapiens"
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/clone="CS0DC06YB08"
/tissue_type="NEUROBLASTOMA"
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/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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Best Local Similarity 98.6%; Pred. No. 5e-179;
Matches 873; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
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Db 64 GCATGTTGAAGAGGTCGTGTCGTCCTCATCGGAGATGTCATCATCCTCTGCGAGT 123
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DEFINITION
AL524358 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
cDNA clone CS0DC06YB08 3-PRIME, mRNA sequence.
ACCESSION
AL524358
VERSION
AL524358.2 GI:31042619
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 949)
AUTHORS
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
COMMENT
On Feb 13, 2001 this sequence version replaced gi:12787851.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster S245.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC06DA04NP1&cluster=5245.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DC06DA04NP1.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
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/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      189 a   255 c   303 g   185 t   17 others
ORIGIN
Query Match      31.9%; Score 869.4; DB 9; Length 949;
Best Local Similarity 96.5%; Pred. No. 5.4e-178;
Matches 893; Conservative 13; Mismatches 17; Indels 2; Gaps 2;
Qy 1750 CCACACTGGAAGACGCCACCCACAGTGCCCAACAGCCAGGCGCCCTGCTGCGC 1809
Db 949 CAACACTGGAAGACGCCACCCACAGTGCCCAACAGCCAGGCGCCGAA-SCYVCTGGCC 891
Qy 1810 CCACCTGTGTCAGATTTGGGGCAAGGCTGAGGGGGACCTACTCTCCCTCTCTCT 1869
Db 890 CCACCTGTGTCAGATTTGGGGCAAGGCTGAGGGGGACCTACTCTCTCCCTCTCTCT 832
Qy 1870 CCATGCTGTCCTGTGGGCTCACACCGGCACTGTGCACTTCTCTCGAGATCCCAT 1929
Db 831 CCATGCTGTCCTGTGGGCTCACACCGGCACTGTGCACTTCTCTCGAGATCCCAT 772
Qy 1930 GGAACAGCCTGCAACGCCCAAGGATGAAGGGGCCAGACACAGCCCTGCTGAGACACGG 1989
Db 771 GGRACAGCCTGCAACGCCCAAGGATGAAGGGGCCAGACACAGCCCTGCTGAGACACGG 712
Qy 1990 TCAATCAGCCTTCTTCCCGCAGGGTCCCTGTCATGGCTGAGAGGGTGTGGGTGCCCTG 2049
Db 711 TCCAATCAGCCTTCTTCCCGCAGGGTCCCTGTCATGGCTGAGAGGGTGTGGGTGCCCTG 652
```

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Qy 2050 TTGACCTACCTGGACCGAGTGGACACGACCTCGCTCCATTAAACCCGGCTGACTCACT 2109
Db |||||
Qy 651 TTGACCTACCTGGACCGAGTGGACACGACCTCGCTCCATTAAACCCGGCTAATCACT 592
Db |||||
Qy 2110 GCAGGAGACACCCGCGACAGTGGTCCAGGGTCCAGCCCTCCGCGAGCCCTGTTCCGCTCA 2169
Db |||||
Qy 591 GCAGGAGACACCCGCGACAGTGGTCCAGGGTCCAGCCCTCCGCGAGCCCTGTTCCGCTCA 532
Db |||||
Qy 2170 CTGGGTGTGGCTTCTGGGACAGGACCAATGCTGGGCGGGGTGFGAATCACGG 2229
Db |||||
Qy 531 CTGGGTGTGGCTTCTGGGACAGGACCAATGCTGGGCGGGGTGFGAATCACGG 472
Db |||||
Qy 2230 GAACGCCCGCGCCCGCCCGCTGCTCCCGGTGTGCAGCGGGTGGCGGTGCGCTTAA 2289
Db |||||
Qy 471 GAACGCCCGCGCCCGCCCGCTGCTCCCGGTGTGCAGCGGGTGGCGGTGCGCTTAA 412
Db |||||
Qy 2290 CATTTCCCTGCTAGTGGCTGCTGTTTACAGTGGGCGCTTCCCTGCGACGGAGGAGG 2349
Db |||||
Qy 411 CATTTCCCTGCTAGTGGCTGCTGTTTTCAGTGGGCGCTTCCCTGCGACGGAGGAGG 352
Db |||||
Qy 2350 ACCAGGCATTAGTCTAGTCTAGAGACTCGCTCGGAAATTTGCTCCATTCTGAGTAAACAG 2409
Db |||||
Qy 351 ACCAGGCATTAGTCTAGTCTAGTCTAGTCTCGCTGGGAAATTTGCTCCATTCTGARTAAACAR 292
Db |||||
Qy 2410 ATATTTCGCCACCTAAAGGAAAGCCTGACCAACTATCACCAAAAGACGAGGCGGC 2469
Db |||||
Qy 291 ATATTTCGCCACCTAAAGGAAAGCCTTAAACAACTATCACCAAAAGACGAGGCGGC 232
Db |||||
Qy 2470 AAAGATTCAGAGCGGGCTTCTGGGCGCGGTTCACAGTGGGCGGTTCCTGCGACGGAGGAGG 2529
Db |||||
Qy 231 AAAGATTCAGAGCGGGCTTCTGGGCGCGGTTCACAGTGGGCGGTTCCTGCGACGGAGGAGG 172
Db |||||
Qy 2530 TTGCTTCTGCGGTGGGCGGAGCGCTGAACAGACCGGGGTGGAGTCAGGGCTGTGCTT 2589
Db |||||
Qy 171 TTGCTTCTGCGGTGGGCGGAGCGCTGAACAGACCGGGGTGGAGTCAGGGCTGTGCTT 112
Db |||||
Qy 2590 TCCGGGTGGTCTGCGCTAGGAGTGGCTTGGGCGGGCCATTTCATTCCTGACC 2649
Db |||||
Qy 111 TCCGGGTGGTCTGCGCTAGGAGTGGCTTGGGCGGGCCATTTCATTCCTGACC 52
Db |||||
Qy 2650 CTCACCTTTCTCATCTGTAAACCA 2674
Db |||||
Qy 51 CTAATTTTCTCATCTKTAACCA 27
Db |||||

RESULT 11
AL517920/c
LOCUS
DEFINITION
AL517920 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CSODA004YB14 3-PRIME, mRNA sequence.
ACCESSION
AL517920
VERSION
AL517920.2 GI:30535708
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12781413.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5245.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODA004DA07NP1&cluster=5245.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVivoGen Corporation 1600
```

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Faraday Avenue Genoscope sequence ID : CSODA004DA07NP1.
Location/Qualifiers
1. 1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODA004YB14"
/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/notes="Vector: pCMVSPORT6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 220 a 314 c 371 g 226 t 70 others
ORIGIN
Query Match 31.7%; Score 864.2; DB 9; Length 1201;
Best Local Similarity 93.5%; Pred. No. 7.9e-177;
Matches 910; Conservative 28; Mismatches 30; Indels 5; Gaps 4;
Qy 1732 CCCTGCCCAAGGTCATCTCCACACTGGAAGAGCCACCCACAGTCCCCCACCAGCCAGG 1791
Db |||||
Qy 968 SCCTCTGCCCAAGTCWTYTTCAAAYT-GAAGAGCCCAACCCACAGT-CCCCACCAGCCAGG 911
Db |||||
Qy 1792 GCGAAGCCCTGTGTGCCCCACCCGTTGTGTCAGCATTTGGTGGGGGCAAGGCTCAGGGGGA 1851
Db |||||
Qy 910 --CCGAACCCYGTGTCGCCACCTGTTTTCAGCATTTGGKGGKGCAGAGGCTGA-GGGGA 854
Db |||||
Qy 1852 CTTACTCTCTCCCTCCCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1911
Db |||||
Qy 853 CCCACVCTTCCCTCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 794
Db |||||
Qy 1912 CTCTGCGACGATCCCTCCATGGAACAGCCCTGACGCGCCAGAGATGAAGGGGCGCAGACCCAGC 1971
Db |||||
Qy 793 YTYTGCGACGATCCCTCCATGAACAGCCCTGTCATGCCAGGATGAAGGGGCGRGSRCSC 734
Db |||||
Qy 1972 CCCTCCCTTGAGACACAGGTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2031
Db |||||
Qy 733 CCCTGCCCTGAGACACAGGTCCCAATCAGCTTCTTCCCCAGGGTCCCTGCTGCTGCTGCTGCT 674
Db |||||
Qy 2032 GAGGGTGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2091
Db |||||
Qy 673 GAGGGTGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 614
Db |||||
Qy 2092 AAACCCGGCTGACTCAGTGCAGGACAGCCCGCACAGTGTGCTCAGGGTCCAGGCCCTCCGC 2151
Db |||||
Qy 613 AAACCCGGCTGACTCAGTGCAGGACAGCCCTGTCAGTGTGCTCAGGGTCCAGGCCCTCCGC 554
Db |||||
Qy 2152 CAGCCCTGTTCCGGCTCACTGGGTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2211
Db |||||
Qy 553 CAGCCCTGTTCCGGCTCACTGGGTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 494
Db |||||
Qy 2212 GGGGTGTGAATATCACCGGGAACGCCCGCCCGCCCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 2271
Db |||||
Qy 493 GGGGTGTGAATATCACCGGGAACGCCCGCCCGCCCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
Db |||||
Qy 2272 GTGGGGTGGCGCTTAAACATTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2331
Db |||||
Qy 433 GGGGGGTGGCGCTTAAACATTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 374
Db |||||
Qy 2332 CCCTGCGACGAGGAGGACGAGCATTAGCTAGTTAGAGACTCGCTGGGAAATTTGCT 2391
Db |||||
Qy 373 CCCTGCGACGAGGAGGACGAGCATTAGCTAGTTAGAGAACTCGCTGGGAAATTTGCT 314
Db |||||
Qy 2392 CCATTCTCTGATTAACAGATATTTTCCCACTAAAGGAGCCCTTGACCAACAACTATC 2451
Db |||||
Qy 313 CCATTCTCTGATTAACAGATATTTTCCCACTAAAGGAGCCCTTAACAACTATC 254
Db |||||
Qy 2452 ACCAAAGACGAGCGCGCAAGATTCAGGGGGCTTCTGCGGCGCGGTTCACAGTGGGT 2511
Db |||||
Qy 253 ACCAAAGACGAGCGCGCAAGATTCAGGGGGCTTCTGCGGCGCGGTTCACAGTGGGT 194
Db |||||
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QY 2512 GGAATTATAGCAGCAGCTTCTCTCTGCGGTCGGGCGCAGCGCTGAACAGACCGGGGT 2571
Db 193 GGAATTATAGCAGCAGCTTCTCTCTGCGGTCGGGCGCAGCGCTGAACAGACCGGGGT 134
QY 2572 GGAGTCAGGCGTGTCTTTCCGCGGTGTTCTGCACATTAGGAGTGTGCGCTTGGCGGGC 2631
Db 133 GGAGTCAGGCGTGTCTTTCCGCGGTGTTCTGCACATTAGGAGTGTGCGCTTGGCGGGC 74
QY 2632 CATTTCACATCTCTGACCCCTCACCTTTCTCATCTGTAAACACAGGCTGATGCCGTGCGGG 2691
Db 73 CNTNTCACATCTCTGACCCCTMACATATCTCATCTGTAAACACAGGCTGATGCCGTGCGGG 14
QY 2692 CTAATGACCCAAAT 2704
Db 13 CTAATGACCCAAW 1

RESULT 12
AL525922
LOCUS
DEFINITION AL525922 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
cDNA clone CS0DC015VF07 5-PRIME, mRNA sequence.
ACCESSION AL525922
VERSION AL525922.2 GI:31063786
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 974)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12789415.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5245.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC015CC04QP1&cluster=5245.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC015CC04QP1.
FEATURES
source
Location/Qualifiers
1..974
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC015VF07"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 199 a 310 c 278 g 183 t 4 others
ORIGIN
Query Match 31.4%; Score 855.6; DB 9; Length 974;
Best Local Similarity 98.8%; Pred. No. 5.4e-175;
Matches 869; Conservative 3; Mismatches 7; Indels 1; Gaps 1;
QY 37 GGGAGGAGCCTTCATGTACAGCAGCAGAGTGGCCATCTTCCTGGTCACTCGTGGCGCG 96
Db 63 GGATGGCAGCCTTCATGTACAGCAGCAGAGTGGCCATCTTCCTGGTCACTCGTGGCGCG 122
QY 97 CACTGACGGGCTCGGCTCCCGGTAGAGCCCTCCCTCATCATCCCCCTGACCCCGG 156
Db 123 CACTGACGGGCTCGGCKKCCCGGTAGAGCCCTCCCTCATCATCCCCCTGACCCCGG 182
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QY 157 AGGGGTCCCTGGAGCTCTCATGGAATGTACAGTACACCCAGGAGGCCATCCATTTCCAGC 216
Db 183 A-GGGTCCCTGGAGCTCTCATGGAATGTACAGTACACCCAGGAGGCCATCCATTTCCAGC 241
QY 217 TCCTGGTCCGAGGCTCAAGGCTGCGCTCTGTTTGGATGTCCGACCGTGGCAGCTTG 276
Db 242 TCCTGGTCCGAGGCTCAAGGCTGCGCTCTGTTTGGATGTCCGACCGTGGCAGCTTG 301
QY 277 AGAAGCAGAGATCTCTGGTGTCTGGACCGATGGGACACCTATTTTCGGACGCGCT 336
Db 302 AGAAGCAGAGATCTCTGGTGTCTGGACCGATGGGACACCTATTTTCGGACGCGCT 361
QY 337 GGAGTGACCAAGAGGGGCGAGATCCACCTGGATCCCCAGCAGGACTACAGCTGTGCAGG 396
Db 362 GGAGTGACCAAGAGGGGCGAGATCCACCTGGATCCCCAGCAGGACTACAGCTGTGCAGG 421
QY 397 TGCAGAGACCCCAAGAGGCTGACCTCTCTTTCAAGAGGCCCTTTGGACCTTCGAGCC 456
Db 422 TGCAGAGACCCCAAGAGGCTGACCTCTCTTTCAAGAGGCCCTTTGGACCTTCGAGCC 481
QY 457 CCAAGGATTACCTCATTTGAAGAGCGGCACTGTCCACTTTGGTCTACGGGATCCTGGAGGAGC 516
Db 482 CCAAGGATTACCTCATTTGAAGAGCGGCACTGTCCACTTTGGTCTACGGGATCCTGGAGGAGC 541
QY 517 CGTTCCGGTCACTGGAGGCCATCAACGGCTCGGGCTGCAGATGGGGCTGCAGAGGGTGC 576
Db 542 CGTTCCGGTCACTGGAGGCCATCAACGGCTCGGGCTGCAGATGGGGCTGCAGAGGGTGC 601
QY 577 AGCTCTGAAGCCCAATATCCCGAAGCGGAGTTGCCCTCAGACGCGTGACCATTTGAGG 636
Db 602 AGCTCTGAAGCCCAATATCCCGAAGCGGAGTTGCCCTCAGACGCGTGACCATTTGAGG 661
QY 637 TCCAAGCTCCCAATATCCAGATCCCGACGAGGACCACTACTGTGTCTACATTAAGG 696
Db 662 TCCAAGCTCCCAATATCCAGATCCCGACGAGGACCACTACTGTGTCTACATTAAGG 721
QY 697 AGCTTCCAAAGGGCTTCTCTCGGCACCACTATTAAGTACGAGGCCCATCGTCAACAGG 756
Db 722 AGCTTCCAAAGGGCTTCTCTCGGCACCACTATTAAGTACGAGGCCCATCGTCAACAGG 781
QY 757 GCAATGAGGCGCTTGTCCACACATGGAAGTCTTTCAGTGGCGCCCGAGATGACAGCG 816
Db 782 GCAATGAGGCGCTTGTCCACACATGGAAGTCTTTCAGTGGCGCCCGAGATGACAGCG 841
QY 817 TCCCCCACTTCAGCGGCGCTCGGACTCCAAAGATGAACCCGACCGCTCAACTACTGCC 876
Db 842 TCCCCCACTTCAGCGGCGCTCGGACTCCAAAGATGAACCCGACCGCTCAACTACTGCC 901
QY 877 GCCACGTGTGGCGCGCTGGGCGCTGGGTGCCAAGGCATT 916
Db 902 GCCACGTGTGGCGCGCTGGGCGCTGGGTGCMARGCATTT 941
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RESULT 13
BX464421
LOCUS
DEFINITION BX464421 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CS0DA004VB14 5-PRIME, mRNA sequence.
ACCESSION BX464421
VERSION BX464421.1 GI:31031625
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 992)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
```

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5245.f For more information about this cluster, see

<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS1DA001ZH10QPl&cluster=5245.f>. Contact : Feng Liang Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS1DA001ZH10QPl.

## FEATURES

Source

1..992 Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DA004YB14"

/tissue\_type="NEUROBLASTOMA"

/clone\_lib="Homo sapiens NEUROBLASTOMA"

/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

BASE COUNT 199 a 280 c 268 g 194 t 51 others

ORIGIN

Query Match

Best Local Similarity 30.7%; Score 837; DB 13; Length 992;

Matches 853; Conservative 44; Mismatches 36; Indels 2; Gaps 2;

QY 88 TGGTGGCGGCGACTGCAGGGCTCGGCTCCCGTGAAGCGCCCTCCCTATCACATCCCC 147  
DB |||||  
QY 148 TGGACCCCGAGGGGTCCTCGAGTCTCATGAATGTCAGTACACCCAGGCGCCATCC 207  
DB |||||  
QY 208 ATTTCCAGTCTCTGGTGGGAGGTCAGGCTGGCTCTGTTGGGATGTCGACCGTG 267  
DB |||||  
QY 268 GCGAGCTTGAAACGAGATCTCTGTGTCTGGACCGATGGGACACACCTATTTTG 327  
DB |||||  
QY 328 CGGACGCTGAGTACAGAGGGGCGAGATCCACCTGGATCCCGCAGGAGCTACGAGC 387  
DB |||||  
QY 388 TGCTGCGAGTGCAGAGACCCAGAGCGCTGACCTGCTTTTCAAGAGCCCTTTGGCA 447  
DB |||||  
QY 448 CCTGCGACCCAGGATTACTCATTAAGACGCGACTGCTGCTTACGGATCC 507  
DB |||||  
QY 508 TGGAGGAGCGCTTCCGGTCACTGAGGCGCATCAACGCTCGGCGCTGCAGATGGGCTGC 567  
DB |||||  
QY 568 AGAGGGTGACGCTTCCAGGCGCAATATCCCGAACCGGAGTGGCCCTCAGACGCTGCA 627  
DB |||||  
QY 628 CCATGAGGTCCAAGTCTCCCAATATCCAGATCCCGACGAGGAGACACGTTACTGTGCT 687  
DB |||||  
QY 688 ACATTAGAGGCTTCCAAAGGGCTTCTTCGGCAACACATTAATCAAGTACGAGCCCATCG 747  
DB |||||  
QY 748 TCACCAAGGCGAATGAGGCCCTTGTCCACACATGGAAGTCTTCCAGTGGCGCCCGGAGA 807

Db 719 TCACCAAGGCGAATGAGGCCCTTGTCCACACATGGAAGTTTTCAGTGGCGCCCGARA 778  
QY |||||  
Db 808 TGGACAGCGTCCCCACTTCAGCGGGCCCTGCAGCTCCAGATGAACCCGCGCTCA 867  
QY |||||  
Db 779 TGGACAGCGTCCCCACTTCAGCGGGCCCTGCAGCTCCAGATGAACCCGCGCTCA 838  
QY |||||  
Db 868 ACTACTGCCGCCACAGTCTGGCGCCCT-GGGCGCTGGTCCCAAGGCATTTTACTACCCA 926  
QY |||||  
Db 839 ACTACTGCCGCCACAGTCTGGCGCCCTKGGGCCCYGGTGCMAAGGATTTAMWAMCMA 898  
QY |||||  
Db 927 GAGGAAGCGCGCTTGCCTTCGGGGCTCAGGGTCTCCAGATATCTCCGCTGGAAGTT 986  
QY |||||  
Db 899 AARRAGCGMGCCCTTTCTTGGGGTTCAGGGTCTT-CAAAAATWTCCGCTKGRAGTT 957  
QY |||||

## RESULT 14

AL526131/c

LOCUS

DEFINITION

AL526131 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens

ACCESSION

AL526131

VERSION

AL526131.2

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

On Feb 13, 2001 this sequence version replaced gi:12789624.

Contact: Genoscope

Genoscope - Centre National de Sequenage

BP 191 91006 EVRY cedex - France

Email: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr). Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5245.f For

more information about this cluster, see

<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DC015CF04NPL&cluster=5245.f>. Contact :Feng Liang Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL :<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DC015CC04NPL.

Location/Qualifiers

1..966

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DC015VF07"

/tissue\_type="NEUROBLASTOMA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoRV

sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 185 a 276 c 320 g 176 t 9 others

ORIGIN

Query Match

Best Local Similarity 30.5%; Score 830; DB 9; Length 966;

Matches 874; Conservative 5; Mismatches 7; Indels 4; Gaps 4;

QY 1809 CCCACCGCTTGTCAGCATTTGGTGGGGCAAAAGGCTGAGGGGAGCTACTCTCCCTCC 1868  
DB |||||  
QY 888 CCCACCGCTTGTCAGCATTTGGTGGGGCAAAAGGCTGAGGGGAGCTACTCTCCCTCC 831  
DB |||||  
QY 1869 TCCATGTGTCCTGTGGGCTCAACCGGCACTGTGCACTTACTCTGCGAGCATCCCA 1928

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Db 830 TCCATGCTGTCCCTGTGGCTCACACCGGCACTGTGCACTCTACTCTCGACGATCCCA 771
Qy 1929 TGGAAACAGCCCTGACGCGCCAGGATGAAGGGCCAGACACAGCCCTCCCTGAGACACAG 1988
Db 770 TGGAAACAGCCCTGACGCGCCAGGATGAAGGGCCAGACACAGCCCTCCCTGAGACACAG 711
Qy 1989 GTCCAAATCCAGCCTTCTT - CCCCCAGGTCCTCTGATGCTGGTGAAGAGGTGTGGTGCC 2047
Db 710 GTCCAAATCCAGCCTTCTT - CCCCCAGGTCCTCTGATGCTGGTGAAGAGGTGTGGTGCC 651
Qy 2048 TGTTCACCTACCTGACCGAGTGAACACAGCCTCTGATTTAAACCCGGCTGACTCA 2107
Db 650 TGTTCACCTACCTGACCGAGTGAACACAGCCTCTGATTTAAACCCGGCTGACTCA 591
Qy 2108 GTGACGGACAGCCGACAGTGTTCAGGGTTCAGCCCTCCGCGAGCCCTGTTCCGGCT 2167
Db 590 GTGACGGACAGCCGACAGTGTTCAGGGTTCAGCCCTCCGCGAGCCCTGTTCCGGCT 531
Qy 2168 CACTGGGTGTGGCTTCTTGGGACAGGACCAATGCTGGGCCGGGTGTGGAATCACC 2227
Db 530 CACTGGGTGTGGCTTCTTGGGACAGGACCAATGCTGGGCCGGGTGTGGAATCACC 471
Qy 2228 GGGAAACGCCCCCGCCCGCTGCTCCGGTGTGACGGGTGGGGTGGCGCTTA 2287
Db 470 GGGAAACGCCCCCGCCCGCTGCTCCGGTGTGACGGGTGGGGTGGCGCTTA 411
Qy 2288 AACATTTCCCTGCTGAGTGGCTGCTTTTACAGTGGCGGCTTCCCTGCGACGGAGCA 2347
Db 410 AACATTTCCCTGCTGAGTGGCTGCTTTTACAGTGGCGGCTTCCCTGCGACGGAGCA 351
Qy 2348 GGACAGGCAATTTAGCTAGTTAGAGACTCGCTGGGAAATTTCTCCTGAGTAAAC 2407
Db 350 GGACAGGCAATTTAGCTAGTTAGAGACTCGCTGGGAAATTTCTCCTGAGTAAAC 291
Qy 2408 AGATATTTCCGCCACCTAAAGGAGCCCTGACAACTATACCAAAAGACGAGCG 2467
Db 290 AGATATTTCCGCCACCTAAAGGAGCCCTGACAACTATACCAAAAGACGAGCG 231
Qy 2468 GCAAAGATCCAGCGGGCTTCTGGCGCGCGGTTCACGTGGGGTGGAAATTTATAGCACCA 2527
Db 230 GCAAAGATCCAGCGGGCTTCTGGCGCGCGGTTCACGTGGGGTGGAAATTTATAGCACCA 171
Qy 2528 GCTTGTCTTCTGCGGTGGGGCCAGCGCTGAAACAGACCGGGGTGGAGTCAAGGCTGTGC 2587
Db 170 GCTTGTCTTCTGCGGTGGGGCCAGCGCTGAAACAGACCGGGGTGGAGTCAAGGCTGTGC 111
Qy 2588 TTTCCGGGTGTTCTGCGCACTTAGGAGTGTGCTTGGCGGGGCCAATTTCACTTCCTGA 2647
Db 110 TTTCCGGGTGTTCTGCGCACTTAGGAGTGTGCTTGGCGGGGCCAATTTCACTTCCTGA 51
Qy 2648 CCCTCACTTTTCTCATCTGTAACCAACGAGCT-GATGCGGTGGGGCTAAT 2696
Db 50 CCCTCACTTTTCTCATCTGTAACCAACGAGCTAGATGCGGTGGGGCTAAT 1
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RESULT 15
BX430865
LOCUS BX430865 874 bp mRNA linear EST 15-MAY-2003
DEFINITION BX430865 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
ClonBB016ZH02 5-PRIME, mRNA sequence.
ACCESSION BX430865
VERSION BX430865
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 874)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
```

Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 5604.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0BAF001ZA04\_AF00026\_1&cluster=5604.f.  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
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Library was not normalized."  
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TITLE			
National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL			
Unpublished			
COMMENT			
Contact: Robert Strausberg, Ph.D.			
Email: cgabs-x@mail.nih.gov			
Tissue Procurement: ATCC			
cDNA Library Preparation: Rubin Laboratory			
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by: Agencourt Bioscience Corporation			
Clone distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LLNL at:			
http://image.llnl.gov			
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insert size 1.8kb. Library constructed by Ling Hong in			
the laboratory of Gerald M. Rubin (University of			
California, Berkeley) using ZAP-cDNA synthesis kit			
(Stratagene) and Superscript II RT (Life Technologies).			
Note: this is a NIH_MGC Library."			
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189 a 339 c 281 g 175 t			
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JOURNAL			
Unpublished			
COMMENT			
Contact: Robert Strausberg, Ph.D.			
Email: cgabs-x@mail.nih.gov			
Tissue Procurement: ATCC			
cDNA Library Preparation: Rubin Laboratory			
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by: Agencourt Bioscience Corporation			
Clone distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LLNL at:			
http://image.llnl.gov			
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EcoRI; cDNA made by oligo-dT priming. Directionally			
cloned into EcoRI/XhoI sites using the following 5'			
adaptor: GGCACGAG(G). Size-selected >500bp for average			
insert size 1.8kb. Library constructed by Ling Hong in			
the laboratory of Gerald M. Rubin (University of			
California, Berkeley) using ZAP-cDNA synthesis kit			
(Stratagene) and Superscript II RT (Life Technologies).			
Note: this is a NIH_MGC Library."			
BASE COUNT			
ORIGIN			
189 a 339 c 281 g 175 t			
Query Match			
Best Local Similarity 29.8%; Score 812.2; DB 13; Length 984;			
Matches 870; Conservative 0; Mismatches 38; Indels 5; Gaps 3;			
QY			
1 TCAGTCCTGGCCAGCCTCCCGGCCCAAGATGCGGAGGAGCGCTTCATGTACAGCA			
60			

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 943)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished

Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)

Tissue Procurement: Dr. James R. Lupski  
cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

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library, non-amplified. Library constructed by Life  
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
College of Medicine); available through Life  
Technologies."

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199 a 324 c 252 g 166 t 2 others

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Qy 580 TCCTGAAGCCCAATATCCCGAACCGGAGTTGCCCTCAGAGCGCTGCACCATGAGGTCC 639

Db 181 TCCTGAAGCCCAATATCCCGAACCGGAGTTGCCCTCAGAGCGCTGCACCATGAGGTCC 240

Qy 640 AAGCTCCCAATATCCAGATCCCGACCGAGGACCACTGTCTGTGTGTACATTAAAGGAGC 699

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Qy 700 TTCCAAAGGGCTTCTCTCGGCACACATATTCAAGTAGAGGCCCATCGTCACCAAGGGCA 759

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Qy 760 ATGAGGCCCTTGTCCACACATGAAGTCTTCCAGTGGCCCCCGAGATGCACAGCGTCC 819

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LOCUS

DEFINITION

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AGENCOURT 8294403 Lupski\_sympathetic\_trunk Homo sapiens cDNA clone  
IMAGE:6194209 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Dr. James R. Lupski  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
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FEATURES

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Directionally cloned using the following adaptors: 5'-TCGACCACGCTCCG-3' and 5'-GACATGTTCTAGATCGGAGCGCCGCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."									
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 ORGANISM Homo sapiens  
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 REFERENCE 1 (bases 1 to 853)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Dr. James R. Lupski  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
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<http://image.llnl.gov>  
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 1 kb for average insert length 1.9 kb. This is a primary  
 library, non-amplified. Library constructed by Life  
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine); available through Life  
 Technologies."

BASE COUNT 176 a 283 c 241 g 153 t  
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Query Match 27.9%; Score 760.2; DB 13; Length 853;  
 Best Local Similarity 96.2%; Pred. No. 2.5e-154;  
 Matches 801; Conservative 0; Mismatches 28; Indels 4; Gaps 2;

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Qy 856 CCGACCGCCTCAACTACTGCGGCCACGTGTCGGCCCTCGGGCCCTGGGTGCCAAGGCAT 915  
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Qy 976 GCTTGGAGTTCTACTACCAACCCACTGGTGTAGTAGAGCAACACGACTCCTCAGGCA 1035  
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QY 1036 TCCGCTTGTACTACACAGCAAGCTGCGCGCTTCAACCGGGGATCATGGAGCTGGAC 1095
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QY 1396 ACACGGAAAGACCGGAGCTGGCCACAGTGGGGGCTTCGGGATCCTGGAGAGATGTGTG 1455
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QY 1515 GCGGCTTCTTCAGAAAGTACTTCCACTCATCAACAGGTTCAACAGAGGATCTGTC 1574
Db 730 GCGGCTTCTTCAGAAAGTACTTCCACTCATCAACAGGTTCAACAGAGGATCTGTC 789
QY 1575 ACCTGCCCTCAGGCG---TCGGTGTCTCAGCAGTTTCACTCTGTTCCTCGGAA 1624
Db 790 CCGTGCCCCCTAGGCGCTCGGGCTCCCAAGTTTCACTCTGTTCCTCGGAA 842
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DEFINITION AGENCOURT 8109142 Lupski sympthetic trunk Homo sapiens cDNA clone
IMAGE:6189465 5', mRNA sequence.
ACCESSION BQ719089.1 GI:21857986
VERSION BQ719089.1
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13586 row: 1 column: 10
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Location/Qualifiers
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Note: Vector: pCMV-SPORT6 (Life Technologies); Site 1:
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACATAGTTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies.
BASE COUNT 182 a 290 c 245 g 151 t 1 others
ORIGIN
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Best Local Similarity 96.9%; Pred. No. 1.4e-150;
Matches 789; Conservative 0; Mismatches 21; Indels 4; Gaps 3;
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QY 390 CTGAGGTGACAGAGGAGCCCGAGAGGCTGACCTGCTTTTCAAGAGGCCCTTTGGCACC 449
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Db 181 TGCACCCCAAGGATTACCTCATTAAGAGCGGACTGTCCACTTGGTCTACGGGATCTCG 240
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Db 241 GAGAGCGCTTTCGGTCACTGGAGGCCATCAACCGGCTCGGGCTGCGAGATGGGCTGCG 300
QY 570 AGGTGAGCTCTCTGAAGCCCAATATCCCGAACCGGAGTTGCCCTCAGACGCTGCACC 629
Db 301 AGGTGAGCTCTCTGAAGCCCAATATCCCGAACCGGAGTTGCCCTCAGACGCTGCACC 360
QY 630 ATGGAGTCCAAAGCTCCCAATATCCAGATCCCGAGCCAGAGACACGTACTGTGTAC 689
Db 361 ATGGAGTCCAAAGCTCCCAATATCCAGATCCCGAGCCAGAGACACGTACTGTGTAC 420
QY 690 ATTAAGAGCTTCAAAGGCTTCTCTCGGCACCAATATCAAGTACGAGCCCATCGTC 749
Db 421 ATTAAGAGCTTCAAAGGCTTCTCTCGGCACCAATATCAAGTACGAGCCCATCGTC 480
QY 750 ACCAAGGCAATGAGGCCCTTGTCCACACATGGAAGTCTTCAGTGGGCCCCCGAGATG 809
Db 481 ACCAAGGCAATGAGGCCCTTGTCCACACATGGAAGTCTTCAGTGGGCCCCCGAGATG 540
QY 810 GACAGCTCCCGCACTTTTCAGCGGCCCTTCAGACTCCCAAGATGAACCCGACCGCTCAAC 869
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
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 Location/Qualifiers

# FEATURES

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 /clone\_lib="NIH\_MGC\_19"  
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Query Match 26.2%; Score 714.4; DB 10; Length 922;  
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 Matches 796; Conservative 0; Mismatches 56; Indels 8; Gaps 4;  
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 Db 2 GCGGCCCTGGACTCCAAAGTGAACCGCGCCCTCAACTACTGCGCGCACGTCGTGG 61  
 QY 889 CCGCTGGCCCTGGGTCCCAAGGCATTTTACTACCCAGAGGAGCGCCCTTGCCTTCG 948  
 Db 62 CCGCTGGCCCTGGGTCCCAAGGCATTTTACTACCCAGAGGAGCGCCCTTGCCTTCG 121  
 QY 949 GGGTCCAGGGTCTCCAGATATCTCCGCTGGGAAGTTCTATACCAACCACTGTTGA 1008  
 Db 122 GGGTCCAGGGTCTCCAGATATCTCCGCTGGGAAGTTCTATACCAACCACTGTTGA 181  
 QY 1009 TAGAAGGACGAAACGACTCCTCAGCATCCCTGTGTACTACACGCAAGCTGGCGGCT 1068  
 Db 182 TAGAAGGACGAAACGACTCCTCAGCATCCCTGTGTACTACACGCAAGCTGGCGGCT 241  
 QY 1069 TCAACGCGGGGATCATGGAGCTGGGACTGGTGTATACCGCCAGTGTATGCCATTCCACCAC 1128  
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 QY 1129 GGGAGACCGCCTTATCTCTCACTGCTACTGCAGGACAAAGTGCACCCAGCTGGCACTGC 1188  
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 QY 1189 CTCCTCCGGGATCCACATCTTCGCTCTCAGCTCCACACACACTGACTGGGAGAAGG 1248  
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 VERSION BX412000.1 GI:30649380  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 947)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 5245.f For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0BAK007CG02NM1&cluster=5245.f. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
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 Library was not normalized."  
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 Query Match 26.0%; Score 709.2; DB 13; Length 947;  
 Best Local Similarity 92.7%; Pred. No. 3e-143;  
 Matches 777; Conservative 0; Mismatches 58; Indels 3; Gaps 3;  
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 QY 1918 GAGATCCCCATGACAGCCCTGCGCCAGATGAAGGGCCACACCGCCCTGC 1977  
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 QY 1978 CTGAGACACGGTCCCAATCCAGCCTTCTTCCCCAGGGTCCCCCTGCATGGCTGAGAGGT 2037

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VERSION BF313609.1 GI:11261645
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 824)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-f@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
BASE COUNT 178 a 262 c 229 g 155 t
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Best Local Similarity 99.1%; Pred. No. 1.9e-140;
Matches 742; Conservative 0; Mismatches 3; Indels 4; Gaps 4;
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QY 1548 AACAGGTTCAACAAACGAGGATCTGCAC 1576
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ACCESSION BG683014
VERSION BG683014.1 GI:13914411
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 905)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Cloned by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW1615 row: b column: 19
High quality sequence stop: 698.
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EcoRI; cDNA made by oligo-dr priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACAGCAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene), and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 182 a 295 c 263 g 165 t
ORIGIN

Query Match 25.3%; Score 690.6; DB 10; Length 905;
Best Local Similarity 94.7%; Pred. NO. 3.2e-139;
Matches 791; Conservative 0; Mismatches 34; Indels 10; Gaps 7;

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QY 181 ATGTTCAGCTACACCCAGGAGCCATCCATTTTCAGCTTCCTGTCGGGAGGCTCAAGCTG 240
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188 ATGTTCAGCTACACCCAGGAGCCATCCATTTTCAGCTTCCTGTCGGGAGGCTCAAGCTG 247

FEATURES
source
/organism="Homo sapiens"

RESULT 26
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cDNA clone CS0DC012YJ10 3-PRIME, mRNA sequence.
ACCESSION AL525638
VERSION AL525638.2 GI:31063502
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 808)
Li,W.B., Gruber,C., Jesses,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12789131.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5245.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC012DE05NP1&cluster=5245.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DC012DE05NP1.
Location/Qualifiers
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/organism="Homo sapiens"

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BASE COUNT 149 a 217 c 285 g 143 t 14 others  
ORIGIN

Query Match 25.3%; Score 689; DB 9; Length 808;  
Best Local Similarity 97.4%; Pred. No. 6.8e-139;  
Matches 702; Conservative 7; Mismatches 10; Indels 2; Gaps 1;  
QY 1693 CCTCAGCCGTCGCTTCCAGGGTGAATGGAACCTGAGCCCTCGCCCAAGGTCTATCTCCA 1752  
DB |||||||  
721 CCTCAGCCGTCGCTTCCAGAGTGAATGGAACCTGAGCCCTCGCCCAAGGTCTATCTCCA 662  
QY 1753 CACTGGAAGAGCCACCCACACAGTGCCTCCACAGCAGGCGCGAGCCCTGCTGGCCCCA 1812  
DB |||||||  
661 CACTGGAAGAGCCACCCACACAGTGCCTCCACAGCAGGCGCGAGCCCTGCTGGCCCCA 602  
QY 1813 CCGTTGTACAGATTGCTGGGGGCAAGGCTGAGGGGGACCTACTCTCTCCCTCTCTCCA 1872  
DB |||||||  
601 CCGTTGTACAGATTGCTGGGGGCAAGGCTGAGGGGGACCTACTCTCTCCCTCTCTCCA 542  
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DB |||||||  
541 TGCTGTCTCTGTGGCTCACACCGGCACTGCACTCTACTCTGGGAGATCCCATGGA 482  
QY 1933 ACAGCCCTGACGCCAGGATGAAGGGGCCAGACACGCCCCCTGCTGAGACCAACGCTCC 1992  
DB |||||||  
481 ACAGCCCTGACGCCAGGATGAAGGGGCCAGACACGCCCCCTGCTGAGACCAACGCTCC 422  
QY 1993 AATCAGCCTTCTTCCCCCAGGGTCCCTGATGGCTGAGAGGTGTGGGTGCGCTTTG 2052  
DB |||||||  
421 AATCAGCCTTCTTCCCCCAGGGTCCCTGATGGCTGAGAGGTGTGGGTGCGCTTTG 362  
QY 2053 ACCTACCTGACCGAGTGGACACAGCTCTGCTCCATTAAACCCGGCTGACTCAGTGCA 2112  
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361 ACCTACCTGACCGAGTGGACACAGCTCTGCTCCATTAAACCCGGCTGACTCAGTGCA 302  
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DB |||||||  
301 GGGACAGCCCAAGTGTCCAGGGTCCAGGGTCCGGCCCTCCCGCAGCCCTGTTCCGGCTCACTG 242  
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DB |||||||  
181 CGCCCCCGCCCCCGCTGCTTCCCGGTGTGTCAGCGGGTGGGGTGGCGTTAAACAT 122  
QY 2293 TTCCCTGCTGAGTGGCTGTTTTCAGTGGGGGCTTCCCTGCGACGAGGACGAGCC 2352  
DB |||||||  
121 TTCCCTGCTGAGTGGCTGTTTTCAGTGGGGGCTTCCCTGCGACGAGGACGAGCC 62  
QY 2353 AGGCATTAGCTAGTAGACTCGCTGGGAAATTGCTCCATTCTCTGAGTAAACAGATA 2412  
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61 AGGCATTAGCTAGTAGACTCGCTGG--AAATGCTCCATTTCNNWAAAWADATA 4  
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DB 3 T 3

RESULT 27  
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LOCUS  
DEFINITION 603635129F1 NIH\_MGC\_47 Homo sapiens cDNA clone IMAGE:5434471 5',

mRNA sequence.  
BM013385  
EST. BM013385.1 GI:16527739  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
AUTHORS 1 (bases 1 to 916)  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
CDNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLC1911 row: j column: 08  
High quality sequence stop: 696.  
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/clone\_lib="NIH\_MGC\_47"  
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."  
BASE COUNT 163 a 308 c 270 g 175 t  
ORIGIN

Query Match 24.7%; Score 673.6; DB 12; Length 916;  
Best Local Similarity 96.9%; Pred. No. 1.6e-135;  
Matches 719; Conservative 0; Mismatches 19; Indels 4; Gaps 3;  
QY 1691 GTCTTCAGCCCTCCGCTTCCAGGGTGAATGGAACCTGAGCCCTCGCCCAAGGTCTATCTC 1750  
DB |||||||  
1 GTCTTCAGCCCTCGCTTCCAGGGTGAATGGAACCTGAGCCCTCGCCCAAGGTCTATCTC 60  
QY 1751 CACTTGAAGAGCCACCCACACAGTGCCTCCACAGCAGGCGCGAAGCCCTGCTGGCCC 1810  
DB |||||||  
61 CACACTGGAAGAGCCACCCACACAGTGCCTCCACAGCAGGCGCGAAGCCCTGCTGGCCC 120  
QY 1811 CACCGTGTCTAGCATTGGTGGGCGAAGCTGAGGGGGACCTACTCTCCCTCCCTCTC 1870  
DB |||||||  
121 CACCGTGTCTAGCATTGGTGGGCGAAGCTGAGGGGGACCTACTCTCTCCCTCCCTCTC 180  
QY 1871 CATGCTGTCCCTGTGGGCTCACACCGGCACCTGTGCACTTACTCTGCGAGATCCCATG 1930  
DB |||||||  
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QY 1931 GAACAGCCCTGACGCGCCAGGATGAAGGGGCCAGACACGCCCCCTGCTGAGACCAAGGT 1990  
DB |||||||  
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QY 1991 CCAATCCAGCCTTCTTCCCCCAGGGTCCCTGATGCTGAGAGGTGTGGGTGCGCTGT 2050  
DB |||||||  
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Db 361 TGACCTACCTCGGACCGAGTGGACACGACCTCGTCCATTTAAACCCGGCTGACTCAGTG 420  
Qy 2111 CAGGACAGCGCGACAGTGGTCCAGGCTCCAGCCCTCCGCGAGCCCTGTTCCGCTCAC 2170  
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Qy 2171 TGGGTGTGGCTGGCTTCTGGGACAGGACCATGCTGG-GCCGGGGTGTGAATCAACCGG 2229  
Db 481 TGGGTGTGGCTGGCTTCTGGGACAGGACCATGCTGGTGGTGGGGTGTGAATCAACCGG 540  
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Db 601 CATTTCCCTGCTGAGTGGCTGCTGTTTCCAGTGGGGGGCTTCCCTTGCACGAGGCC 660  
Qy 2347 AGGACCGAGCATTTAGCTAGTGTAGAGACTCGCTGGGAAATTGTCTCAATTCCTGAGTAAA 2406  
Db 661 AGGACCGAGCATTTAGCTAGTGTAGAGACTCGCTGGGAAATTGTCTCAATTCCTGAGTAAA 720  
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Db 721 CAGATATTTTCCGCCACCTAAA 742

## RESULT 28

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LOCUS 601895945F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:4125395 5',  
DEFINITION mRNA sequence.

ACCESSION BF315987  
VERSION BF315987.1 GI:11264277

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 764)

NIH-MGC <http://mgs.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)

Plate: LUCM1013 row: 1 column: 12

High quality sequence stop: 719.

Location/Qualifiers

## FEATURES

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/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCAGGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

BASE COUNT  
ORIGIN

Query Match 24.7%; Score 672.8; DB 10; Length 764;  
Best Local Similarity 96.9%; Pred. No. 2.2e-135;  
Matches 729; Conservative 0; Mismatches 17; Indels 6; Gaps 4;

Qy 707 GGGCTTCTCTCGGCACACATTTATCAAGTACGAGCCCATCTCAACAGGCAATGAGGC 766  
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Qy 767 CTTTGTCCACACATGGAAGTCTTCCAGTGGCCCGCCGAGATGACAGCGTCCCCACTT 826  
Db 61 CTTTGTCCACACATGGAAGTCTTCCAGTGGCCCGCCGAGATGACAGCGTCCCCACTT 120

Qy 827 CAGCGGCGCTTCCAGTCCCAAGATGAACCCGACCGCTCAACTACTGCCGCCACGTGCT 886  
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Qy 887 GGCGCGCTTGGGCTTCCAGTGGTCCAAAGGATTTTACTACCCAGAGGAAGCCGCCCTTGCCTT 946  
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Qy 947 CGGGGGTCCAGGGTCCCTCAGATATCTCCGCTTGGAGTTTCACTACCAACACCCACTGGT 1006  
Db 241 CGGGGGTCCA-GGTCTCTCCAGATATCTCCGCTTGGAGTTTCACTACCAACACCCACTGGT 299

Qy 1007 GATAGAAGGACGAAACGACTCTCAGGCATCCGCTTGTACTACACAGCAAGCTGCGGCG 1066  
Db 300 GATAGAAGGACGAAACGACTCTCAGGCATCCGCTTGTACTACACAGCAAGCTGCGGCG 359

Qy 1067 CTTCAACCGCGGGATCATGAGCTGGAGCTGGGTGTACACGCCAGTATGGCCATTCCACC 1126  
Db 360 CTTCAACCGCGGGATCATGAGCTGGAGCTGGGTGTACACGCCAGTATGGCCATTCCACC 419

Qy 1127 ACGGAGACCGCTTCTCATCTCTCAGTCTGCTACTCAGCAGACAGTGCACCCAGCTGGCACT 1186  
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Qy 1187 GCCTCCCTCCGGGATCCACATCTTCGCTCTCAGCTCCACACACACCTGACTGGGAGAAA 1246  
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Qy 1247 GGTGGTCAAGTGTCTGTCGGGACCGCGGAGTGGGAGATCGTG-AACAGGACAAATC 1305  
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Qy 1366 GAGATGTGCTCATCACCCTCTGCACGTACAACAGGAGACCGGGAGTGGSCCAGAGTGG 1425  
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RESULT 29  
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DEFINITION 603634780F1 NIH\_MGC\_47 Homo sapiens cDNA clone IMAGE:5421955 5',  
mRNA sequence.

ACCESSION BM011085

VERSION BM011085.1 GI:16525439

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 875)

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)



Matches 699; Conservative 0; Mismatches 3; Indels 3; Gaps 3;  
QY 1846 GGGGGACCTACTCTCCCTCCCTCTCCATGCTGTCTCCCTGTGGGCTCACACCGGCACTGTGC 1905  
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8 GGGGGACCTACTCTCTCCCTCCCTCTCCATGCTGTCTCCCTGTGGGCTCACACCGGCACTGTGC 67  
QY 1906 ACTTACTCTGCGAGCATCCCATCGAATGGAACAGCCCTGCAAGCCGAGATGAAGGGGCCAGA 1965  
Db ACTTACTCTGCGAGCATCCCATGGAACAGCCCTGCAAGCCGAGATGAAGGGGCCAGA 127  
QY 1966 CCAGCCCTCTGCTGAGACCAAGGTCGAATCCAGCTTCTTCCCGGAGTCCCTGTCAT 2025  
Db CCAGCCCTCTGCTGAGACCAAGGTCGAATCCAGCTTCTTCCCGGAGTCCCTGTCAT 187  
QY 2026 GGCTGAGAGGGTGGGGTCCCTGTTGACCTACCTGACCGAGTGGACCAACGACCTCGT 2085  
Db GGCTGAGAGGGTGGGGTCCCTGTTGACCTACCTGACCGAGTGGACCAACGACCTCGT 247  
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Db CCAITTAACCGGCTGACTAGTGCAGGAGCAGCCGCGACAGTGGTCCA-GGTCCAGCC 306  
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Db CTCGCCAGCCCTGTTCCGCTCTACTGGGTGGGCTTCTGGGACGACCACTGC 365  
QY 2206 TGGGCGGGGTGTGGAATCACCGGAAACGCGCCCGCCCGCTGCTCCCGGTGTG 2265  
Db TGGGCGGGGTGTGGAATCACCGGAAACGCGCCCGCCCGCTGCTCCCGGTGTG 425  
QY 2266 CAGCGGTGGGGTGGCGCTTAACATTTCCCTGCTGAGTGGCTGTTTCAAGTGGG 2325  
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QY 2326 CGGCTTCCCTGCGAGGAGGAGGACGAGGATTTAGTAGTGGGACTCGCTGGAA 2385  
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Db ATTGCTCATTTCTGAGTAACAGATATTTTCG-CCACCTAAAGGAGGCTTGCACAACA 604  
QY 2446 ACTATCAACAAAGACGAGGCGCAAGATCCAGGGGGCTTCTGGGCGCGGTTCACAG 2505  
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RESULT 31  
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LOCUS  
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mRNA sequence.  
ACCESSION BE382698  
VERSION BE382698.1 GI:9328063  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 713)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)  
Plate: LLCM310 row: n column: 17  
High quality sequence stop: 660.  
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/tissue\_type="neuroblastoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_19"  
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."  
BASE COUNT 154 a 243 c 189 g 127 t

Query Match 24.2%; Score 658.4; DB 10; Length 713;  
Best Local Similarity 96.6%; Pred. No. 2.8e-132;  
Matches 684; Conservative 0; Mismatches 21; Indels 3; Gaps 1;  
QY 548 GGGGCTCAGATGGGGCTGCAGAGGGTGCAGCTCTGAGGCCAATATCCCGAACCGGA 607  
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QY 608 GTTCCCTCAGACGCGTGCACCATGAGGCTCCAGCTCCCAATATCCAGATCCCGACCA 667  
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QY 1088 GCTGGGACTGGTGTACACGCAAGTGGCCATTTCCACCGGGAGACCGCTTATCCT 1147  
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Db 601 CACTGGCTACTGCACGCAAGTGGCCATTTCCACCGGGAGACCGCTTATCCT 660  
QY 1208 CTTCCGCTCTCAGCTCCACACACACCTGACTGGGAGAAAGTGTGTAC 1255

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Db      661 TCTTCGCTCAG---TCCACACACTGATGGAGACGGTGGCCCC 705
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ACCESSION      AL525444
VERSION      AL525444.2 GI:31063308
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 817)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12788937.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5245.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC012DE05QP1&cluster=5245.f. Contact :
Feng Liang Email: fliang@life.techn.com URL :
http://fulllength.invitrogen.com/InvitroGen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DC012DE05QP1.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC012YJ10"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/prime="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      157 a 257 c 240 g 154 t 9 others
ORIGIN
source
Query Match      23.3%; Score 633.8; DB 9; Length 817;
Best Local Similarity 99.5%; Pred. No. 64e-127;
Matches 646; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY      1 TCAGTCGCTGGCCAGAGCTGCGGCCGCCAGCATGCGGGAGGAGCGCTTCATGTACAGCA 60
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QY      61 CAGCAGTGGCCATCTTCTGTGATCTCTGTGCGCCAGCTGAGGCTGGCTCCCGTG 120
Db      135 CAGCAGTGGCCATCTTCTGTGATCTCTGTGCGCCAGCTGAGGCTGGCTCCCGTG 194
QY      121 AGAGCCCTCTCCCTATFACATCCCTCGGACCGGAGGCGTCCCTGGAGCTCTCATGGA 180
Db      195 AGAGCCCTCTCCCTATFACATCCCTCGGACCGGAGGCGTCCCTGGAGCTCTCATGGA 253
QY      181 ATGTGACACTACCCAGAGGCGCATCCATTTCCAGCTCTCTGTGCGGAGGCTCAAGGCTG 240
Db      254 ATGTGACACTACCCAGAGGCGCATCCATTTCCAGCTCTCTGTGCGGAGGCTCAAGGCTG 313
QY      241 GCGTCTGTTTGGATGTGCGACCGTGGGAGCTTGAGAACCGAGATCTCGGTGGTCTCT 300
Db      314 GCGTCTGTTTGGATGTGCGACCGTGGGAGCTTGAGAACCGAGATCTCGGTGGTCTCT 373
QY      301 GGACCGATGGGACACTGCTATTTTGGCGGACGCTGAGTGAACGAGGAGGCGAGATCC 360
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Db      374 GGACCGATGGGACACTGCTATTTTGGCGGACGCTGAGTGAACGAGGAGGCGAGATCC 433
QY      361 ACCTGGATCCCGCAGCAGGACTACAGCTGTGCGAGTGCAGAGGAGCCCGAAGGCGCTGA 420
Db      434 ACCTGGATCCCGCAGCAGGACTACAGCTGTGCGAGTGCAGAGGAGCCCGAAGGCGCTGA 493
QY      421 CCCTGCTTTTCAAGAGGCGCTTTGGGACCTGCGACCCCGAGGATTACCTCATTTGAAGACG 480
Db      494 CCCTGCTTTTCAAGAGGCGCTTTGGGACCTGCGACCCCGAGGATTACCTCATTTGAAGACG 553
QY      481 GCATGTCTCACTTGGTCTACGGGATCCTGGAGGAGCGGTTCCCGTCACTGGAGGCCATCA 540
Db      554 GCATGTCTCACTTGGTCTACGGGATCCTGGAGGAGCGGTTCCCGTCACTGGAGGCCATCA 613
QY      541 ACCGCTCGGCGCTGCAGATGGGCTGCAGAGGCTGCAGCTCTTGAAGCCCAATATCCCCG 600
Db      614 ACCGCTCGGCGCTGCAGATGGGCTGCAGAGGCTGCAGCTCTTGAAGCCCAATATCCCCG 673
QY      601 AACCGAGTTGCCCTCAGACGCGTGCACCATGGAGGTCCCAAGCTCCCAA 649
Db      674 AACCGAGTTGCCCTCAGACGCGTGCACCATGGAGGTCCCAAGCTCCCAA 722
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BF311746      945 bp mRNA linear EST 21-NOV-2000
LOCUS      BF311746
DEFINITION      601897245F1 NIH_MGC_19 Homo sapiens CDNA clone IMAGE:4126571 5',
mRNA sequence.
ACCESSION      BF311746
VERSION      BF311746.1 GI:11259506
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 945)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW1016 row: j column: 12
High quality sequence stop: 732.
Location/Qualifiers
1..945
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/clone="IMAGE:4126571"
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/lab_host="DH10B (phage-resistant)"
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/notes="Organ: brain; Vector: pOT7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adapter: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
Note: This is a NIH MGC Library."
BASE COUNT      207 a 300 c 277 g 161 t
ORIGIN
source
Query Match      23.2%; Score 633; DB 10; Length 945;
Best Local Similarity 90.8%; Pred. No. 1e-126;
Matches 767; Conservative 0; Mismatches 60; Indels 18; Gaps 8;
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QY 707 GGGCTTCTCTCGGCACCACTTATCAAGTACGAGCCCATCGTCACCAAGGCGCAATGAGGC 766  
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QY 767 CTTTGTCCACCATGGAAGTCTTCAGTGGCGCCCGAGATGGACAGGCTCCCACTT 826  
Db 61 CTTTGTCCACCATGGAAGTCTTCAGTGGCGCCCGAGATGGACAGGCTCCCACTT 120  
QY 827 CAGCGGGGCTCGGACTCAAGATGAACCCGACCGCTCAACTACTGCGCGCAGTGCT 886  
Db 121 CAGCGGGGCTCGGACTCAAGATGAACCCGACCGCTCAACTACTGCGCGCAGTGCT 180  
QY 887 GCGCGCTTGGGCTTGGTGGCAAGGCAATTTTACTACCCAGAGGAGCGGCTTGGCTT 946  
Db 181 GCGCGCTTGGGCTTGGTGGCAAGGCAATTTTACTACCCAGAGGAGCGGCTTGGCTT 240  
QY 947 CCGGGTCCAGGCTCTCAGATATCTCGGCTCGAAGTTCTACTACCAACCACTGGT 1006  
Db 241 CCGGGTCCCA-GGTCTCAGATATCTCGGCTCGAAGTTCTACTACCAACCACTGGT 299  
QY 1007 GATAGAAGGACGAAACGACTCTCAGGATCGCTTGTACTACAGACCAAGCTCGGCG 1066  
Db 300 GATAGAAGGACGAAACGACTCTCAGGATCGCTTGTACTACAGACCAAGCTCGGCG 359  
QY 1067 TTCAACCGGGGATCATGGAGCTGGGACTGGTGTACACGCGAGTGATGGCCATTCAC 1126  
Db 360 TTCAACCGGGGATCATGGAGCTGGGACTGGTGTACACGCGAGTGATGGCCATTCAC 419  
QY 1127 ACGGAGACCGCTTCTCCTCAGTCTGCTACTGACGAGCAAGTGACCCAGCTGGCACT 1186  
Db 420 ACGGAGACCGCTTCTCCTCAGTCTGCTACTGACGAGCAAGTGACCCAGCTGGCACT 479  
QY 1187 GCCTCCCTCGGGATCCACATCTTCGCTCTCAGCTCCACACACACCTGCTGGGAGAA 1246  
Db 480 GCCTCCCTCGGGATCCACATCTTCGCTCTCAGCTCCACACACACCTGCTGGGAGAA 538  
QY 1247 GGTGTACAGTGTGTGTCGGGAGCGCGGAGTGGGAGATCGTGAACACGAGCAATCA 1306  
Db 539 GGTGTACAGTGTGTGTCGGGAGCGCGGAGTGGGAGATCGTGAACACGAGCAATCA 598  
QY 1307 CTACAGCCCTCATTCCAGGAGATCC-GCATGTTGAAGAAGTGTGTGCGTCCATCCGG 1365  
Db 599 CTACAGCCCTCATTCCAGGAGATCCGGCATGTTGAAGAAGTGTGTGCGTCCATCC 658  
QY 1366 GAGATG-----TGCTCATACCTCTGACGCTACACACGGA-GACCGGAGCTGG- 1416  
Db 659 GGGAGATGTGCTCATCAACCTCTGCGACGTACACACGGAAGGACCGGAGCTGGG 718  
QY 1417 -CCAGTGGGGGCTTCGGGATCCTG---GAGGAGATGTGTCAACTAGT--GCACT 1470  
Db 719 CCACAGTGGGGGCTTCGGGATCCTGGAGGAGATGGGGTGTCCACTAAGTTGCACTA 778  
QY 1471 ACTACCCCAAGCAGCAGCTGAGCTCTGCAAGACGGTGTGGACCGCGCTTCTGCGAGA 1530  
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QY 1531 AGTAC 1535  
Db 839 ATTCC 843

RESULT 34  
LOCUS BF316475  
DEFINITION BF316475 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:4131041 5',  
mRNA sequence.  
ACCESSION BF316475  
VERSION BF316475.1 GI:11264832  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 759)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Sequencing by: Incyte Genomics, Inc.  
Cloned through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: LCM1028 row: d column: 18  
High quality sequence stop: 670.  
Location/Qualifiers  
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/clone="IMAGE:4131041"  
/tissue\_type="neuroblastoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_19"  
/note="Organ: Brain; Vector: pOTB7; Site: 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCAGGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH MGC Library."  
BASE COUNT 165 a 253 c 204 g 137 t  
ORIGIN

Query Match 23.2%; Score 631.8; DB 10; Length 759;  
Best Local Similarity 96.0%; Pred. No. 1.7e-126;  
Matches 723; Conservative 0; Mismatches 22; Indels 8; Gaps 7;  
QY 530 GGAGGCCATCAACGGCTCGGGCTCGAGATGGGGCTGCAGAGGGTGCAGCTCTGTAAGCC 589  
Db 2 GGAGGCCATCAACGGCTCGGGCTCGAGATGGGGCTGCAGAGGGTGCAGCTCTGTAAGCC 61  
QY 590 CAATATATCCCAAGCCGAGTGTGCTCAGACGCGTGACCATGAGGTCCCAAGCTCCCAA 649  
Db 62 CAATATATCCCAAGCCGAGTGTGCTCAGACGCGTGACCATGAGGTCCCAAGCTCCCAA 121  
QY 650 TATCCAGATCCCAAGCCGAGGAGACCATGCTACTGTGTCTACATTAA-GGAGCTTCCAAAG 708  
Db 122 TATCCAGATCCCAAGCCGAGGAGACCATGCTACTGTGTCTACATTAAAGCGAGCTTCCAAAG 181  
QY 709 GCTTCTCTCGCACCATATTAAGTACGAGCCCATGTCACCAAGGGCAATGAGGCC 768  
Db 182 GCTTCTCTCGCACCATATTAAGTACGAGCCCATGTCACCAAGGGCAATGAGGCC 241  
QY 769 TTGTCCACCATGGAAGTCTTCCAGTGGCGCCCGGAGATGGACA-GGGTCCCGCACCTTC 827  
Db 242 TTGTCCACCATGGAAGTCTTCCAGTGGCGCCCGGAGATGGACATGTGTCCCGCACCTTC 301  
QY 828 AGC--GGGCGCTCGGACTTCCAAAGATGAACCC--GACCGCTTCAACTACTGCGCGCACGTG 884  
Db 302 AGCTGTGTGCTCGGACTTCCAAAGATGAACCCCTGACCGCTTCAACTACTGCGCGCACGTG 361  
QY 885 CTGCGCGCTTGGGCTTGGTGGCCAAAGCATTTTACTACCCAGAGGAGCGGCTTGGC 944  
Db 362 CTGCGCGCTTGGGCTTGGTGGCCAAAGCATTTTACTACCCAGAGGAGCGGCTTGGC 421  
QY 945 TTGCGGGGTTCAGGGTCTCTCCAGATATCTCGCGCTGGAAGTTTCACTACCAACCCACTG 1004  
Db 422 TTGCGGGGTTCAGGGTCTCTCCAGATATCTCGCGCTGGAAGTTTCACTACCAACCCACTG 481  
QY 1005 GTGATAGA-AGGACGAAACGACTCTCTCAGGATCCGCTTGTACTACAGCAAGCTGCG 1063

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Db      482 GTGATAGACGAGCAAGAAACGACTCTCTCAGGATCCGCTTGACTACACAGCCAGCTGGC 541
QY      1064 GCGCTTCAACGGGGGATCATGGAGCTGGAGCTGGTGTACACGCCAGTATGCCATTTC 1123
Db      542 GCGCTTCAACGGGGGATCATGGAGCTGGAGCTGGTGTACACGCCAGTATGCCATTTC 601
QY      1124 ACCACGGGAGACCGCTTTCATCTCTCACTGGCTACTGACGAGCAAGTGCACCCAGCTGGC 1183
Db      602 ACCACGGGAGACCGCTTTCATCTCTCACTGGCTACTGACGAGCAAGTGCACCCAGCTGGC 661
QY      1184 ACTGCTCCCTCCGGATCCACATCTTGGCTCTCAGCTCCACACACACTGACTGGGAG 1243
Db      662 ACTGGCTCCCTCCGGATCCACATCTTGG-CTCTAGCTCACACACACTGACTGGGAG 720
QY      1244 AAAGGTGGTACAGTGTCTGTCGGGACGGCG 1276
Db      721 AACGGTGGAC-CAGTGTGTTCGGGACGGCG 752

RESULT 35
LOCUS   BX411774/c
DEFINITION BX411774 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
ACCESSION BX411774
VERSION   BX411774
KEYWORDS  BX411774.1 GI:30763182
SOURCE   EST.
ORGANISM Homo sapiens (human)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL   Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
COMMENT   Full-length cDNA libraries and normalization
          Unpublished
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          Bp 191 91006 EVRY cedex - France
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          Library was constructed by Life Technologies, a division of
          Invitrogen. This sequence belongs to sequence cluster 5245.f For
          more information about this cluster, see
          http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAK003CA12NM1&cluster=5245.f. Contact :
          Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/Invitrogen Corporation 1600
          Faraday Avenue Genoscope sequence ID : CS0BAK003CA12NM1.
          Location/Qualifiers
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              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="Cl0BB0112C07"
              /tissue_type="NEUROBLASTOMA"
              /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
              with a NotI-oligo(dT) primer. Five prime end enriched,
              double-strand cDNA was digested with Not I and cloned into
              the Not I and EcoRV sites of the pCMVSPORT 6 vector.
              Library was not normalized."
              172 a 267 c 253 g 216 t

BASE COUNT 172 a 267 c 253 g 216 t
ORIGIN

Query Match 22.8%; Score 621.4; DB 13; Length 908;
Best Local Similarity 91.08; Pred. No. 3.2e-124;
Matches 694; Conservative 0; Mismatches 66; Indels 3; Gaps 3;

QY      1935 AGCCTGCAGCCGAGATGAAGGGCCAGACCCAGCCCGCTGCTGAGACCAAGTCCAA 1994
Db      766 AGCAAGACACAGCCGACCGGAAAGGAAACAAACACATCGTTAAACACGCGACAA 707
QY      1995 TCCAGCTCTTCCCTCCAGGGTCCCTGCATCGCTGAGAGGTGTGGGTGCCTGTTGAC 2054

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Db      706 TACAACTTCTTCCACAGGCTCCCTCGATGAAGGAGAGTGAATGATGATCCCTATTACA 647
QY      2055 CTACCTTGACC-GAGTGGACACGACTCGTCAATTTAAACCCGGCTGACTCAGTGCAG 2113
Db      646 CAACCTTGACCCGAGTGGCCACGGCTCGTCCATTTAAACACAGGCTGACTCAGTGCAG 587
QY      2114 GGACAGCCCGCACAGTGGTCCAGGGTCCAGCCCTCCGCCAGCCCTGTTCCGCTCACTGG 2173
Db      586 GGACAGCTGCACA-TGGTCCAGGGTCCAGCCCTCCGCCAACCCCTGTTCCGCTCACTGG 528
QY      2174 GTGTGGCTGGCTTCTGGGACAGGCACCATGCTGGGCCGGGGTGTGGAATCACCGGGAAC 2233
Db      527 GTGTGGCTGGCTTCTGGGACAGGCACCATGCTGGGCCGGGGTGTGGAATCACCGGGAAC 468
QY      2234 GCCCCCGCCCGCCCGCTGCTCCCGGTGTGACGGGGTGGGGTGCCTTTAAACATT 2293
Db      467 GCACCCCGCCCGAACCGCTGCTCCCGGTGTGACAGGGTGGCGGTGCGCTTAAACATT 408
QY      2294 TCCTGCTGAGTGGCTCGTGTTCACAGTGGGGCGGCTTCCCTGCAGACGAGGACGACCA 2353
Db      407 TCCTGCTGAGTGGCTCGTGTTCACAGTGGGGCGGCTTCCCTGCAGGAGGAGGACCA 348
QY      2354 GGCATTTAGCTAGTTAGAGACTCGCTGGGAATTTGCTCCATTTCTCTGATTAACAGATAT 2413
Db      347 GGCATTTAGCTAGTTAGAGACTCGCTGGGAATTTGCTCCATTTCTCTGATTAACAGATAT 288
QY      2414 TTTGCGCCACCTAAAGGGAAGCCCTGACAAACAATCATCAACAAAGACAGCGGCGCAAG 2473
Db      287 TTTGCGCCACCTAAAGGGAAGCCCTGACAAACAATCATCAACAAAGACAGCGGCGCAAG 228
QY      2474 ATCCAGCGGGCTTTTGGCGCGGTTCCAGTGGGGTGGAAATTTAGCACCACTTTCG 2533
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QY      2534 TTCTCTGCGGTGGGCGCAGCGCTGAACAGACCGGGTGGAGTAGGGCTGTGCTTTCG 2593
Db      167 TTCTCTGCGGTGGGCGCAGCGCTGAACAGACCGGGTGGAGTAGGGCTGTGCTTTCG 108
QY      2594 CTGTGTTTCGCATTAGGAGTGTGCTTGGCGGGGCATTTTCACATTTCTCTGACCTCA 2653
Db      107 CGTGTGTTTCGCATTAGGAGTGTGCTTGGCGGGGCATTTTCACATTTCTCTGACCTCA 48
QY      2654 CTTTCTCATCTGTAAACACGAGCTGATCCGTCGGGCTAAAT 2696
Db      47 CTTTCTCATCTGT-AAACACGAGTGTGCTTGGCGGGGCATTTTCACATTTCTCTGACCTCA 6

RESULT 36
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DEFINITION 601871147F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4101706 5',
ACCESSION BF206759
VERSION   BF206759.1 GI:11100345
KEYWORDS  EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL   NIH-MGC http://mgi.nci.nih.gov/.
COMMENT   National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished
          Contact: Robert Strausberg, Ph.D.
          Email: gnapbs-f@mail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Ling Hong/Rubin Laboratory
          DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
          plate: LLCW873 row: n column: 11
          High quality sequence stop: 720.

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QY      1129 GGGAGCCGCTTCATCTCCTCACTGGCTACTGCAACGAGCAAGTGACCCAGCTGGCACTGC 1188
Db      |||||||
QY      301 GGGAGCCGCTTCATCTCCTCACTGGCTACTGCAACGAGCAAGTGACCCAGCTGGCACTGC 360
Db      |||||||
QY      1189 CTCCTCCCGGATCCACATCTTCGCTCTCACTCCACACACACTGACTGGGAGAAAGG 1248
Db      |||||||
QY      361 CTCCTCCCGGATCCACATCTTCGCTCTCACTCCACACACACTGACTGGGAGAAAGG 420
Db      |||||||
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Db      |||||||
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Db      |||||||
QY      1309 ACAGCCCTCACTTCAGGAGATCCGATGTTGAAGAGTCTGTCGGTCCATCCCGGAG 1368
Db      |||||||
QY      481 ACAGCCCTCACTTCAGGAGATCCGATGTTGAAGAGTCTGTCGGTCCATCCCGGAG 540
Db      |||||||
QY      1369 ATGTGCTCATCTTCCTGCACTACACACGAGACCGGAGTGGAGTGGAGTGGAGTGGAG 1428
Db      |||||||
QY      541 ATGTGCTCATCTTCCTGCACTACACACGAGACCGGAGTGGAGTGGAGTGGAGTGGAG 599
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QY      600 GCTTCGGGATCCTGAGGAGATGTG 626

RESULT 38
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LOCUS      601150168F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502889 5',
DEFINITION mRNA sequence.
ACCESSION BE260752
VERSION   BE260752.1 GI:9132302
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM175 row: g column: 18
High quality sequence stop: 598.
Location/Qualifiers
1. 605
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/db_xref="taxon:9606"
/clone="IMAGE:3502889"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."
119 a 213 c 159 g 114 t
BASE COUNT
ORIGIN

Query Match
22.0%; Score 599.2; DB 10; Length 605;

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Best Local Similarity 99.5%; Pred. No. 1.8e-119;
Matches 601; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      1  AAGGTCGTCGTCGGTCCATCCGGGAGATGTCATCACTCTCTGCACTGCAACACGAA 60
Db      |||||||
QY      1404 GACCGGAGCTGGCCACAGTGGGGGCTTCGGGATCCTGGAGAGATGTCATCACTAC 1463
Db      |||||||
QY      61  GACCGGAGCTGGCCACAGTGGGGGCTTCGGGATCCTGGAGAGATGTCATCACTAC 120
Db      |||||||
QY      1464 GTGCACTACTACCCCCAGAGCGAGCTGTGAAGACGGCTGTGAGCGCGGCTTC 1523
Db      |||||||
QY      121  GTGCACTACTACCCCCAGAGCGAGCTGTGAAGACGGCTGTGAGCGCGGCTTC 180
Db      |||||||
QY      1524 CTGCAAGTACTTCCACACCTCATCAACAGGTTCAACAGGATGTCGCACTGCCCT 1583
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QY      181  CTGCAAGTACTTCCACACCTCATCAACAGGTTCAACAGGATGTCGCACTGCCCT 240
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QY      1584 CAGCGCTCGTGTCTGAGCAGTTCACTGTTCCTGGAACTCTTCAACCGGACGTA 1643
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QY      241  CAGCGTCCGTGTCTGAGCAGTTCACTGTTCCTGGAACTCTTCAACCGGACGTA 300
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QY      301  CTGAAGGCCCTGTACAGCTTCGCGCCATCTCCATGCACTGCAACAGTCTCGACCGTC 360
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QY      361  CGCTTCAGGGTGAATGGAACTGCAAGCCCTGCCCCAGGTCATCTCCACACTGGAAGAG 420
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Db      |||||||
QY      481  ATTGTCGGGGCAAGGCTGAGGGGGACCTACTCTCCCCCTCTCCATGCTGTCCCTG 540
Db      |||||||
QY      1884 TGGGTCACACCGGCACTGTGCACTCTACTCTGAGAGATCCCGATGGAAACGCCCTGCA 1943
Db      |||||||
QY      541  TGGGTCACACCGGCACTGTGCACTCTACTCTGAGAGATCCCGATGGAAACGCCCTGCA 600
Db      |||||||
QY      1944 CGCC 1947
Db      ||||
QY      601 TGCC 604

RESULT 39
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LOCUS      601901840F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4131296 5',
DEFINITION mRNA sequence.
ACCESSION BE316292
VERSION   BE316292.1 GI:11264633
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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      in the laboratory of Gerald M. Rubin (University of
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      Note: this is a NIH_MGC Library."
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  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished
  Contact: Robert Straubeberg, Ph.D.
  Email: csapbs-remail.nih.gov
  Tissue Procurement: ATCC
  cDNA Library Preparation: Ling Hong/Rubin Laboratory
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
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        in the laboratory of Gerald M. Rubin (University of
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